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DNA Deformation by Proteins DNA in Bound and Unbound States

J. Locasale and H. Berman (Rutgers U.)

Beamline(s): X12C

It is well known that DNA bound to protein can adopt radically different conformations relative to canonical DNA structure. But does this distortion arise entirely from structural changes induced by the protein or can this phenomenon be intrinsic to the DNA structure? To fully understand the effects of protein-mediated DNA deformation, a careful analysis of starting and ending conformations is requisite. The Nucleic Acid Database contains over 150 structures of right-handed DNA and over 700 structures of protein-DNA complexes; however, there are very few cases for which there are structures of the bound and unbound DNA. Our project attempts to resolve questions concerning the structural basis of sequence specificity in DNA recognition by comparing DNA in its bound and unbound state. We have crystallized selected DNA oligonucleotides that contain recognition sites for proteins. One particular sequence, 5' GCAGACGTCTGC 3', contains the site, AGACGTCT, to which the methionine repressor protein binds. This sequence has been crystallized along with its derivative, 5' GCAGACGTC(5-Bromo-Uridine)GC 3'. Preliminary diffraction has shown that the brominated derivative is isomorphous with the native sequence. At X12C, we have collected a MAD data with the bromine derivative. Further work is being conducted to